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SELF-SIMILARITY IN THE TAXONOMIC CLASSIFICATION OF HUMAN LANGUAGES

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Statistical properties of the taxonomic classification of human languages are studied. It is shown that, at the highest levels of the taxonomic hierarchy, the frequency of taxon members as a function of the number of languages belonging to each member decays as a power law. This feature reveals that a self-similar structure underlies the taxonomy of languages, exactly as observed in the taxonomic classification of biological species. Such an analogy is a clue to the evolutionary foundation of language classification based on long-range comparison.

1. Introduction

Comparative linguistics shows that human languages can be grouped in a hierarchy of families whose members share a certain level of similarity, much like biological species in the taxonomic tree. This hierarchy is defined in terms of mutual relatedness and affinity of languages in their present form, but also takes into account evolutionary aspects such as common innovations. Ruhlen [1] compiled data for the almost 5,000 extant languages and proposed a taxonomic classification which, at the highest level, consists of 17 families. Some instances of these large families are the Indo-Hittite, which contains all Indo-European languages and is the largest in number of speakers; the Austric, which covers parts of South-Eastern Asia and Oceania and is the richest in number of languages; and the Amerind, which was one of the latest to be recognized as a family [2]. These families are divided into primary branches, which in turn contain groups, subgroups, branches, and so on. Along certain particularly rich branches (e.g. Bantu, in Africa) Ruhlen's classification distinguishes up to 17 hierarchical levels or taxa.

The methods of long-range comparison that make possible the identification of language families at the highest taxonomic levels have been emphatically criticized by many linguists [3,4]. These authors claim that an upper bound of 6,000-8,000

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years exists for the time elapsed from the separation of two languages from a common ancestor such that any connection between them can be established by comparison. Ruhlen's work, however, has received strong support from a field outside linguistics, namely genetics, through detailed studies of the genetic distance between human populations by Cavalli-Sforza and coworkers [5]. These authors have shown that, at the highest levels, the taxonomy of populations is remarkably similar to that of languages. The similarity can be traced up to levels corresponding to the main population expansions towards Eastern Asia, Oceania, and the Americas, some tenths of thousand years ago [6].

In this paper, statistical regularities of the taxonomic classification of languages at the highest taxa are disclosed. The hierarchical distribution of languages is shown to exhibit self-similarity properties, which could hardly be explained if such distribution were derived from a baseless method. Comparison with the case of biological species, in fact, supports an evolutionary basis for the classification of languages.

2. Analysis

Our statistical analysis proceeds as follows. We choose a specific taxon of the hierarchy (say, primary branches). For each member i of that taxon (say, Indo-European) we determine the number n_i of extant languages belonging to that member (for Indo-European, $n_i = 144$). The set of values n_i obtained for the selected taxon is then used to construct a histogram. The height of each column in the histogram is proportional to the fraction of members whose number of languages lies within the interval covered by the column, normalized by the column width. In other words, it gives the frequency $f(n)$ of taxon members which contain a given number n of languages.

Table 1. Statistical parameters of the taxonomic classification. The exponents γ and ν characterize the power-law dependence of the frequency of members of a given taxon on the number of languages and the number of members in the successive taxon, respectively. The regression coefficient measures the quality of the least-square fitting from which γ is obtained.

taxon	exponent γ	regression coefficient	exponent ν
first	1.0 ± 0.2	-0.903	1.0 ± 0.2
second	1.4 ± 0.1	-0.976	1.7 ± 0.1
third	1.6 ± 0.1	-0.990	1.7 ± 0.1
fourth	1.9 ± 0.1	-0.993	1.9 ± 0.1
fifth	2.1 ± 0.1	-0.998	—

Results for the highest, first five taxa (families, primary branches, groups, subgroups, and branches) are presented in Fig. 1. For clarity, the histograms are displayed as sets of points, and the frequencies corresponding to each set are expressed

in arbitrary units. In all cases, the data exhibit a regime of well-defined power-law decay, $f(n) \sim n^{-\gamma}$, spanning more than two decades in the number of languages, typically from $n \approx 2$ to $n \approx 300$, and three to four decades in frequencies. The exponent γ , obtained from linear least-square fitting on the log-log plot, is given for each set in Table 1. The fittings are shown in Fig. 1 as straight lines. As a measure of the fitting quality, the regression coefficients are also given in Table 1. They are always above 0.9 (in modulus).

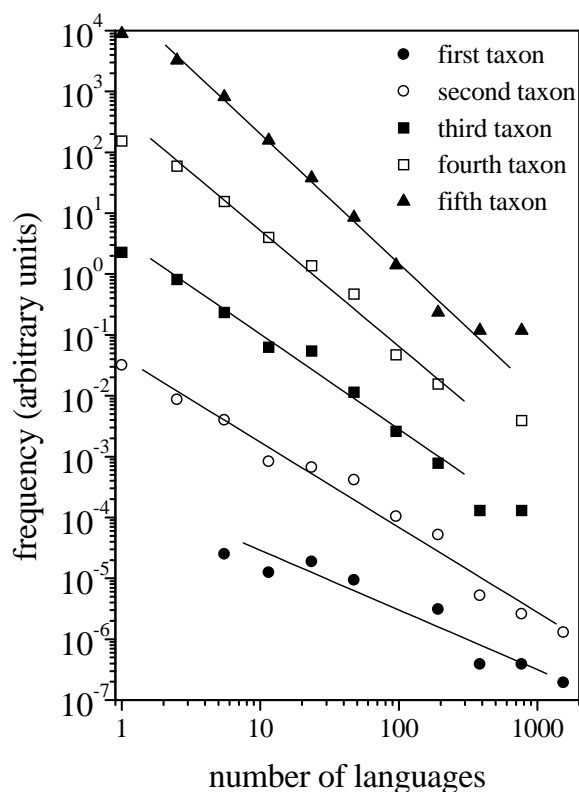


Fig. 1. Frequency of taxon members, shown as a function of the number of languages belonging to each member, for the first five taxonomic levels (families, primary branches, groups, subgroups, and branches). For clarity in displaying, the frequencies of each set have been multiplied by an appropriate constant. The lines correspond to least-square fittings in the intervals where they are plotted.

The regression coefficients show that the definiteness of the power-law dependence improves for lower taxa. This is also apparent from Fig. 1, where the linear approximation is relatively poorer for the first taxa. We ascribe this effect to the fact that the number of members of a given taxon decreases considerably as higher

taxa are considered. For the first taxon, in fact, the (8-column) histogram is constructed from a set of only 17 values. In this specific case, it is more reliable to study the distribution of languages in families using a rank plot [7]. The rank r of a family is given by its place in a list where families are sorted in decreasing order by the number of languages belonging to them ($r = 1$ for the richest family, $r = 2$ for the second richest, and so on). The rank plot displays the number of languages as a function of r , as shown in Fig. 2. In this linear-log plot the straight line stands for an exponential decay, $n \sim \exp(-ar)$, and can be shown to correspond to a frequency of the form $f(n) \sim n^{-1}$. These data are reasonably well approximated by a linear fit (regression coefficient = -0.988), which is in full agreement with the corresponding power-law exponent $\gamma = 1.0 \pm 0.2$, quoted in Table 1.

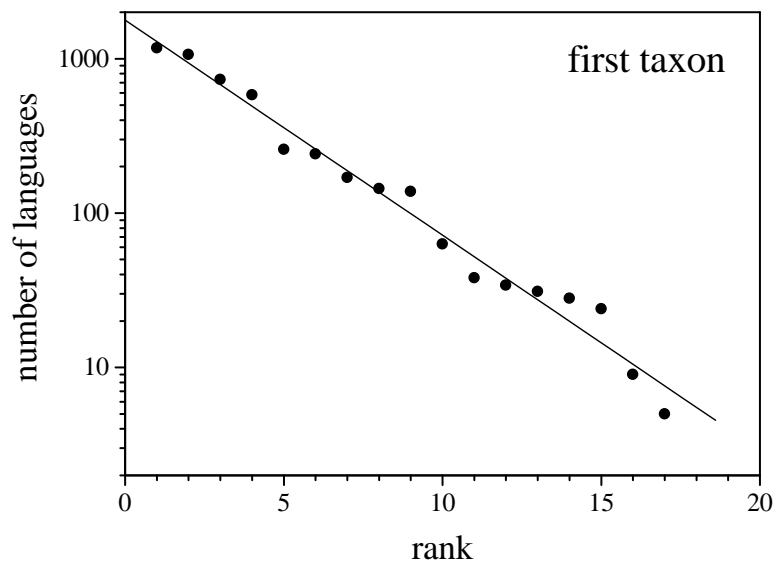


Fig. 2. Rank plot of the first taxon (families). The number of languages belonging to each member is plotted as a function of its rank. The straight line corresponds to an exponential decay and has been determined by least-square fitting.

The fact that the frequency $f(n)$ exhibits power-law dependence for several taxa implies another important statistical property of the taxonomic classification. Consider two consecutive taxa t and $t + 1$ with frequencies $f_t(n) \sim n^{-\gamma}$ and $f_{t+1}(n) \sim n^{-\gamma'}$, respectively, and call $p(m)$ the fraction of members of taxon t that contain a number m of members of the successive taxon $t + 1$. These three

distributions are related through the expression

$$f_t(n) = \sum_m p(m) f_{t+1}(n) \circ f_{t+1}(n) \circ \cdots \circ f_{t+1}(n), \quad (2.1)$$

where the m -th term involves the m -fold discrete convolution of f_{t+1} with itself. In the Laplace domain, this relation reads

$$\phi_t(s) = \sum_m p(m) [\phi_{t+1}(s)]^m \approx \int_0^\infty p(\mu) [\phi_{t+1}(s)]^\mu d\mu, \quad (2.2)$$

where ϕ_t and ϕ_{t+1} are the Laplace transforms of f_t and $f_{t,t+1}$, respectively. In the right-hand side of Eq. (2.2), the variable μ replaces the summation index m to produce a continuous approximation to ϕ_t . The power-law decay of $f_t(n)$ implies that, near $s = 0$, its Laplace transform behaves as $\phi_t(s) \approx \exp(-a|s|^{\gamma-1})$ for $1 < \gamma < 2$ and as $\phi_t(s) \approx \exp(-bs - c|s|^{\gamma-1})$ for $2 < \gamma < 3$, where a , b , and c are constant coefficients [8]. Analogous approximate expressions hold for $\phi_{t+1}(s)$. These asymptotic expressions satisfy the continuous approximation in Eq. (2.2) if the distribution $p(m)$ is in turn a power law for large m , $p(m) \sim m^{-\nu}$. The exponent ν is a function of γ and γ' , namely,

$$\nu = 1 + \frac{\gamma - 1}{\gamma' - 1} \quad (2.3)$$

if $1 < \gamma, \gamma' < 2$, and

$$\nu = \gamma \quad (2.4)$$

if $1 < \gamma < 2 < \gamma'$. Its value for the first four taxa is also given in Table 1.

3. Discussion and conclusion

Power-law frequency distributions are known to reveal self-similarity and fractal geometry in the underlying structures [9] –in our case, the taxonomic tree. The interest of this statistical property of the taxonomic classification of languages resides in the fact that exactly the same feature is found in the taxonomy of biological species. The power-law dependence in the frequency of biological taxon abundance has been first discussed by Yule [10] and, much later, Burlando [11,12] studied in detail the distribution of the exponent ν at different levels and along different branches of the taxonomic tree, also including some families of extinct species. In contrast with the case of languages, the exponent ν for biological taxonomy can directly be measured on the tree. Indeed, the biological taxonomic tree is very rich –it contains more than 1,500,000 species at the lowest level. Even at the highest taxa, one finds members with a large number of members from the successive taxon. On the other hand, the extant languages are less than 5,000. The statistics are consequently much poorer, and the exponent ν is more reliably inferred from the values of γ and γ' , as done above. It has been found that, for biological species, ν varies in a relatively narrow interval, $1.4 < \nu < 2.5$. Note that, except for the first taxon, the values of ν obtained for language taxonomy are also in that interval.

Several models have been proposed to account for the statistical regularities in the taxon abundance of biological species, ranging from branching dynamical processes [10,13,14] to simplified macroevolutionary models [15,16]. Though these stylized models do reproduce the fractal-like structure of taxonomic trees, which suggests that they successfully capture the essential ingredients in the organization of biological taxa, they seldom give a quantitatively satisfactory explanation of such regularities. By now, however, there is little doubt that the power-law distributions found in taxon abundance are a consequence of the inherently complex mechanisms that drive biological macroevolution, giving rise to speciation and, more generally, originating new members at all the taxonomic levels. Self-similarity and fractal features, in fact, have been recognized as a clue to the underlying complexity in a large class of dynamical systems [9]. The fact that the same kind of distributions is found in the taxonomy of languages strongly suggests that language classification reflects, even at its highest levels, the underlying evolutionary mechanisms.

In summary, we have shown that, at the highest levels of the taxonomic classification of human languages, the frequency of members containing a given number of languages decays as a power-law over at least two decades. These systematic regularities seem to discard the possibility that the classification results from a baseless method. Moreover, they imply that the frequency of taxon members containing a given number of members from the successive taxon is also well described by a power-law distribution. The same property is found in the taxonomy of biological species, whose evolutionary origin is firmly established. Along with the genetic evidence provided by Cavalli-Sforza, this analogy supports an evolutionary basis for Ruhlen's classification.

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References

- [1] M. Ruhlen, *A Guide to the World's Languages - Volume 1: Classification*. (Stanford University Press, 1987).
- [2] J. H. Greenberg, *Language in the Americas* (Stanford University Press, 1987).
- [3] T. Kaufman, in *Amazonian Linguistics*, ed. D. Payne (University of Texas Press, Austin, 1990).
- [4] H. H. Hock, *Principles of Historical Linguistics* (Mouton de Gruyter, Berlin, 1991).
- [5] L. L. Cavalli-Sforza, A. Piazza, P. Menozzi, and J. L. Mountain, *Proc. Nat. Acad. Sci. U.S.A.* **85**, 6002 (1988).
- [6] M. Ruhlen, *The Origin of Language* (Wiley, New York, 1994).
- [7] G. K. Zipf, *Human Behavior and the Principle of Least Effort* (Addison-Wesley, Reading, 1949).
- [8] G. Doetsch, *Introduction to the theory and application of the Laplace transform* (Springer, New York, 1994).
- [9] B. Mandelbrot, *Fractals and Self-Affinity* (Springer-Verlag, New York, 1997).

- [10] G. U. Yule, *Proc. R. Soc. London Ser. B* **213**, 21 (1924).
- [11] B. Burlando, *J. theor. Biol.* **146**, 99 (1990).
- [12] B. Burlando, *J. theor. Biol.* **163**, 161 (1993).
- [13] T. Matsumoto and Y. Aizawa, *Prog. Theor. Phys.* **102**, 909 (1999).
- [14] J. Chu and C. Adami, *Proc. Nat. Acad. Sci. U.S.A.* **96**, 15017 (1999).
- [15] R. Solé and S. C. Manrubia, *Phys. Rev.* **E54**, R42 (1996).
- [16] R. Solé and S. C. Manrubia, *Phys. Rev.* **E55**, 4500 (1997).